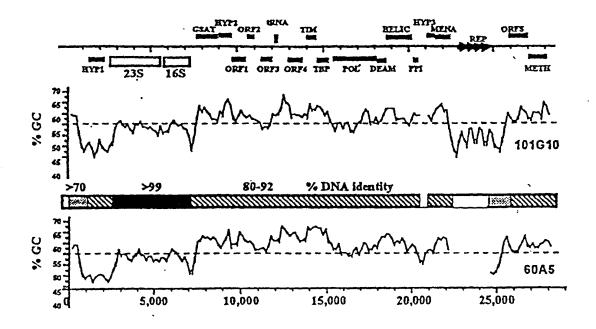
## FIGURE 1



## Figure 2

69 00	Gene	<u>Strain</u>		TATA Box			Coding Start		TATA to Start (bp)	
81 82	Hypoth 03	A B					GCGGCGCATG CCGGCGCGTG			25
83 84	Hypoth 02	A B					CGGGGCCCAT	· ·		26
85 86	ORF 02	A B					AACGGCCGTA ACCTGCCGTA			27
88	ORF 03	A B	CATGGAACTA	GATAAT	AACC	GGTCCCGCGG	ATCCCATGCA GTACAATGCA	TG	~~~~~~~	27
90	PPI	A B	AGCACGACAA	GTTATA	GCAG	GGTACAAAGG	GTGCGCGCGC AGCAGCGCAC	ATG~~~~	~~~~~~~~~~~	28
9.1 92	GSAT	A B	ATCCGGCCTC	ATTAAA	TTAC	GGGGGTACA	GCCTGCTGCC ACCTGCTGCC	GTG~~~~~	~~~~~~~	28
94	ORF 05	A B	ACTTCATACA	CATAAA	TCCC	GCCTGAACGG	GCGGCTGCGC	ATG~~~~~	~~~~~~~	28
96	deaminase	A B	CCGCATATAC	CATAAT	ATGC	CGGGCGGGG	CACCATGGCC CAGGCTGCCC	. GTG~~~~~	~~~~~~~~	29
98	RNA helic	A B A	GGGTAGAAAC	CATAAA	ACAA	CAGGCCGCGG	CAGGGCCGCG CAGGGCG.CG GCGCGTATCA	CGTG	~~~~~~~	29 29
100	tRNA-tyr	B A	ATACACGTGG	TATAAA	CAGA	GG.CCGGACG	GCGCGGACCA CACGGATCGT	CATG	~~~~~~~	29
102 193	TBP	B A	GCGATAGTTA	TTTAAA	ACTA	GGATGCCGGG	CACCCGTCGT GGATCCTGAC	CCCA	~~~~~~	30
105	TIM	B A					GGCACCGGAT CCCGTGGCGC			36
106	Hypoth 01	B A					GCGGTGC GAAATAGCAA			45
108	ORF 01	B A	ACGGCAGGCT	ATTATT	ACCT	TGCCTTGCGT	GAAATATCAA TGTA //G	CGGGGTGCGG	CAGGGGATG	52
	Methylase	B A	CTACAACGAT	TTTAAG	TCGG	CGCCGGGGCA	TACA //G GCCG.//G	ATGTGGGGCA	GGCAACATG	104
112	16S RNA	B A B	TCGGCGATGG	TTTATA	TGCC	CATGGACGGG	GCGG.//T CCGATCCGAT GCGATCCGAT	CGTACGTGAC	GC.//AAT	220
" [	Archaeal promoter consensus			YTTAWA		DIMONOLLE	CCGAICCGAI	COINCUIGNC	00.77.12022	

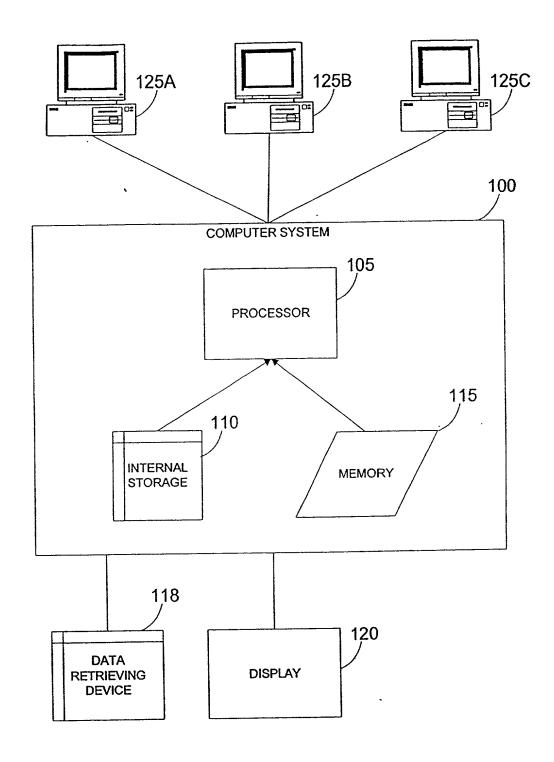


FIGURE 3

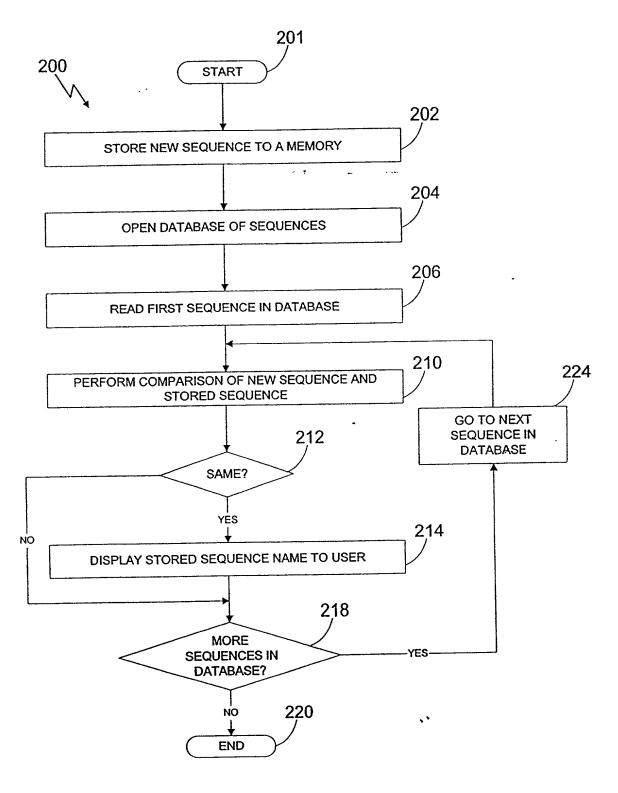


FIGURE. 4

